

SEQUENCE LISTING

<110> Sprecher, Cindy A.
 Presnell, Scott R.
 Gao, Zeren
 Whitmore, Theodore E.
 Kuijper, Joseph L.
 Maurer, Mark F.

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<151> 2000-06-26

<150> US 60/214,955

<151> 2000-06-29

<150> US 60/267,963

<151> 2001-08-02

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Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr	
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Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp	
55 60 65	
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Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser	
70 75 80	
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Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val	
85 90 95	
gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca tac tgg	512
Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp	
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Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val	
115 120 125 130	
aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg ata aag	608
Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys	
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Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe	
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Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn	
165 170 175	

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215 220 225	
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Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser	
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Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu	
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Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr	
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Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu	
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His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu	
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Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val	
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Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys	
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Val	Ser	Pro	Glu	Ile	Pro	Pro	Arg	Lys	Ser	Gln	Tyr	Leu	Arg	Ser	Arg	
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 Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala Pro Asn
 695 700 705

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 Pro Tyr Leu Lys Asn Ser Val Thr Ala Arg Glu Phe Leu Val Ser Glu
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aaa ctt cca gag cac acc aag gga gaa gtc taaatgcgac catagcatga 2386
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 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
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 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65 70 75 80
 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
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 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
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 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
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Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
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 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
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 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
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 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
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 260 265 270
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 275 280 285
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 325 330 335
 Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
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 355 360 365
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 370 375 380
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 ttccaactag gaagactgaa tctgtggccc caagagaacc atctctgaag actgggtatg 1560
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 tctgttatta agtagagtgt gaaaacatgg ttatggtaat aggaacagct tttaaaatgc 1680
 ttttgcattt gggcctttca tacaaaaaag ccataatacc attttcatgt aatgctatac 1740
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<210> 17

<211> 1299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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 aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg 176
 Met Met Trp Thr Trp
 1 5

gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
 10 15 20

cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
 Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
 25 30 35

tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
 40 45 50

aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
 Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
 55 60 65

acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt 416

Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	Phe	Leu	
70					75					80					85	
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Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	Ala	Glu	
				90					95					100		
aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	tta	gag	512
Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	Leu	Glu	
			105					110					115			
aac	ata	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	cca	gtt	560
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Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	Glu	Leu	
	135					140					145					
gcg	cct	gtt	tca	tct	gat	tta	aaa	tac	aca	ctt	cga	ttc	agg	aca	gtc	656
Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val	
150					155					160					165	
aac	agt	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	aag	aac	cgt	aag	gat	704
Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp	
				170				175					180			
aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	752
Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr	
			185					190					195			
gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	800
Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp	
		200					205					210				
tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	gct	cca	tgt	ggc	848
Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly	
	215					220					225					
ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	896
Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg	
230					235					240					245	

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Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu
250 255 260

aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac 992
Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn
265 270 275

ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg 1040
Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu
280 285 290

gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg 1088
Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly
295 300 305

aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa 1133
Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys
310 315 320

tagaaacttt	acagatgcta	gtcccagaca	taaaagaaaa	taatgttctg	gatgtgcacg	1193
atggctcacg	cctgtaatcc	cagcactttg	aggccaagac	gggtggatcg	ctgagttcag	1253
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<213> Homo sapiens

<400> 18

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			20					25					30		
Tyr	Tyr	Arg	Lys	Asn	Leu	Thr	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr
		35					40					45			
Ser	Tyr	Thr	Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys
	50					55					60				
His	Asp	Asn	Cys	Thr	Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser
65					70					75					80
Cys	Ser	Phe	Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile
				85					90					95	

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
 260 265 270
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
 275 280 285
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
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<210> 19

<211> 23

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<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27897

<400> 19

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<210> 20

<211> 22
 <212> DNA
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<220>
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<400> 20
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<210> 21
 <211> 1476
 <212> DNA
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 aaaacattct ctctccccag ccttcattgtg ttaacctggg g atg atg tgg acc tgg 176
 Met Met Trp Thr Trp
 1 5
 gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
 10 15 20
 cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
 Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
 25 30 35
 tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
 40 45 50
 aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
 Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
 55 60 65
 acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt 416

Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	Phe	Leu	
70					75					80					85	
cca	aga	ata	acg	atc	cca	gat	aat	tat	acc	att	gag	gtg	gaa	gct	gaa	464
Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	Ala	Glu	
				90					95					100		
aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	tta	gag	512
Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	Leu	Glu	
			105					110					115			
aac	ata	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	cca	gtt	560
Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	Pro	Val	
		120					125					130				
ttg	ggc	atc	aaa	cga	atg	att	caa	att	gaa	tgg	ata	aag	cct	gag	ttg	608
Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	Glu	Leu	
	135					140					145					
gcg	cct	gtt	tca	tct	gat	tta	aaa	tac	aca	ctt	cga	ttc	agg	aca	gtc	656
Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val	
150					155					160					165	
aac	agt	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	aag	aac	cgt	aag	gat	704
Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp	
				170					175					180		
aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	752
Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr	
			185					190					195			
gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	800
Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp	
		200					205					210				
tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	ggc	aag	cta	ctc	848
Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Gly	Lys	Leu	Leu	
	215					220					225					
cct	gcg	att	ccc	gtc	ctg	tct	gct	ctg	gtg	tagggctgct	ttgggctaga					898
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<213> Homo sapiens
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Ser	Leu	Ala	Ala	Leu	Pro	Ala	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Tyr
			20					25					30		
Tyr	Tyr	Arg	Lys	Asn	Leu	Thr	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr
		35					40					45			
Ser	Tyr	Thr	Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys
	50					55				60					
His	Asp	Asn	Cys	Thr	Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser
65					70					75					80
Cys	Ser	Phe	Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile
			85						90					95	
Glu	Val	Glu	Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr
			100					105					110		
Tyr	Trp	Arg	Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe
		115					120					125			
Arg	Val	Lys	Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp
	130					135				140					
Ile	Lys	Pro	Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu
145					150					155					160
Arg	Phe	Arg	Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala
			165						170					175	
Lys	Asn	Arg	Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln
			180					185					190		
Pro	Phe	Thr	Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser
		195					200					205			

Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
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 Glu Gly Lys Leu Leu Pro Ala Ile Pro Val Leu Ser Ala Leu Val
 225 230 235

<210> 23
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<220>
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<210> 24
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<400> 24
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<210> 25
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<210> 26
 <211> 21
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<220>

<223> Oligonucleotide primer ZC17574

<400> 26

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21

<210> 27

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<223> Oligonucleotide primer ZC17600

<400> 27

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24

<210> 28

<211> 25

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<223> Oligonucleotide primer ZC26358

<400> 28

aaaaccaaac gtacaacctc acggg

25

<210> 29

<211> 25

<212> DNA

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<223> Oligonucleotide primer ZC26359

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<223> Oligonucleotide primer ZC17313

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<223> Oligonucleotide primer ZC17205

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<400> 33

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<212> PRT

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<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> FLAG tag peptide sequence

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1 5

<210> 36

<211> 699

<212> DNA

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acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
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gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccg	ggtaaataa			699

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<211> 990

<212> DNA

T09290" 64625860

<213> Homo sapiens

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<222> (1)...(990)

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agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac	96
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr	
20 25 30	
ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc	144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser	
35 40 45	
ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc	192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser	
50 55 60	
ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc	240
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr	
65 70 75 80	
tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag	288
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys	
85 90 95	
aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc	336
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys	
100 105 110	
cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca	384
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro	
115 120 125	
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc	432
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys	
130 135 140	

"09290" 64626660

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Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
145 150 155 160	
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag	528
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
165 170 175	
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg	576
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
180 185 190	
cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac	624
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
195 200 205	
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg	672
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
210 215 220	
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag	720
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu	
225 230 235 240	
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat	768
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
245 250 255	
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac	816
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
260 265 270	
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc	864
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
275 280 285	
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac	912
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
290 295 300	
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg	960
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990

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<212> PRT
<213> Homo sapiens
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Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
35						40						45				
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	
50						55						60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	
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Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
				85				90				95				
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
				100				105				110				
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
115						120						125				
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
130						135						140				
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
145					150				155				160			
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
				165				170				175				
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
			180						185			190				
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
195						200						205				
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
210						215						220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	
225					230				235				240			
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	
				245				250				255				

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

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 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 39

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 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
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ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 96
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30

ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 144
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45

ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 192
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60

tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 240
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 288

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gtc aca aag agc ttc aac agg gga gag tgt tag
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
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<210> 40
<211> 106
<212> PRT
<213> Homo sapiens
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Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr		
			20					25					30				
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser		
		35				40						45					
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr		
	50					55					60						
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys		
65					70					75					80		
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro		
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Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys								
			100					105									

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<212> DNA
<213> Artificial Sequence
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<223> Oligonucleotide primer ZC11440

<400> 41
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8

<210> 42
<211> 8
<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC11441

<400> 42

cgcgctctc

8

<210> 43

<211> 100

<212> DNA

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<220>

<223> Oligonucleotide primer ZC12749

<400> 43

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aactgtagat ttctaggaat tcaatccttg gccacgcgtc 100

<210> 44

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC12748

<400> 44

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cgcggttgta attccgggaa ggggagggat ttacgggaag 100

<210> 45

<211> 2529

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg	176
Met Met Trp Thr Trp	
1 5	
gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg	224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu	
10 15 20	
cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat	272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn	
25 30 35	
tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac	320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr	
40 45 50	
aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca	368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr	
55 60 65	
acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt	416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu	
70 75 80 85	
cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa	464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu	
90 95 100	
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag	512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu	
105 110 115	
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt	560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val	
120 125 130	
ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg	608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu	
135 140 145	
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc	656

Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val	
150 155 160 165	
aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat	704
Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp	
170 175 180	
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat	752
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr	
185 190 195	
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac	800
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp	
200 205 210	
tgg agc caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc	848
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro Cys Gly	
215 220 225	
ctg gaa ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga aga agg	896
Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg	
230 235 240 245	
cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc cta gag	944
Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu	
250 255 260	
aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac	992
Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn	
265 270 275	
ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg	1040
Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu	
280 285 290	
gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg	1088
Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly	
295 300 305	
aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa tca	1136
Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys Ser	
310 315 320 325	

ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac cag cta	1184
Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu	
330 335 340	
gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg atg att	1232
Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile	
345 350 355	
gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa	1280
Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu	
360 365 370	
tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa	1328
Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys	
375 380 385	
cct ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa	1376
Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys	
390 395 400 405	
gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca	1424
Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro	
410 415 420	
tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc	1472
Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val	
425 430 435	
acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc	1520
Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile	
440 445 450	
tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc	1568
Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser	
455 460 465	
aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa	1616
Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys	
470 475 480 485	
cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt gct ggg	1664

Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser Ala Gly	
490 495 500	
gga acc aac ggg acc agc ata aat ttc aag aca ttg tca ttc agt gtc	1712
Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe Ser Val	
505 510 515	
ttt gag att atc ctc ata act tct ctg att ggt gga ggc ctt ctt att	1760
Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu Leu Ile	
520 525 530	
ctc att atc ctg aca gtg gca tat ggt ctc aaa aaa ccc aac aaa ttg	1808
Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn Lys Leu	
535 540 545	
act cat ctg tgt tgg ccc acc gtt ccc aac cct gct gaa agt agt ata	1856
Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser Ser Ile	
550 555 560 565	
gcc aca tgg cat gga gat gat ttc aag gat aag cta aac ctg aag gag	1904
Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu Lys Glu	
570 575 580	
tct gat gac tct gtg aac aca gaa gac agg atc tta aaa cca tgt tcc	1952
Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser	
585 590 595	
acc ccc agt gac aag ttg gtg att gac aag ttg gtg gtg aac ttt ggg	2000
Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly	
600 605 610	
aat gtt ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa	2048
Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu	
615 620 625	
aac aat tta gga ggg gaa aag aat ggg act aga att ctg tct tcc tgc	2096
Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser Ser Cys	
630 635 640 645	
cca act tca ata taagtgtgga ctaaaatgcg agaaaggtgt cctgtggtct	2148
Pro Thr Ser Ile	

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 agagaaccat ctctgaagac tgggtatgtg gtcttttcca cacatggacc acctacggat 2268
 gcaatctgta atgcatgtgc atgagaagtc tgttattaag tagagtgtga aaacatgggt 2328
 atggtaatag gaacagcttt taaaatgctt ttgtatttgg gcctttcata caaaaaagcc 2388
 ataataccat tttcatgtaa tgctatactt ctatactatt ttcatgtaat actatacttc 2448
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<211> 649

<212> PRT

<213> Homo sapiens

<400> 46

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 35 40 45
 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
 50 55 60
 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65 70 75 80
 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
 85 90 95
 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220

09290"64626860

Glu 225	Ala	Pro	Cys	Gly	Leu 230	Glu	Leu	Trp	Arg	Val 235	Leu	Lys	Pro	Ala	Glu 240
Ala	Asp	Gly	Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp 250	Lys	Lys	Ala	Arg	Gly 255
Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro 260
Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln 275
Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser 290
Tyr	Asn	Ser	Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala 305
Ile	Gln	Glu	Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val 320
Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val 340
Asn	Thr	Trp	Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr 355
Thr	Leu	Ser	Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln 370
Gln	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro 385
Met	Leu	His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala 405
Lys	Glu	Gly	Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile 420
Gly	Val	Lys	Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu 435
Arg	Lys	Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly 450
Gly	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly 465
Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala 485
Ser	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr 500
Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly 515
Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys 530
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<210> 47
<211> 1947
<212> DNA
<213> Artificial Sequence

<220>
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<221> misc_feature
<222> (1)...(1947)
<223> n = A,T,C or G
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acntggwsnc	cnggnaarga	racnwsntay	acncartaya	cngtnaarmg	nacntaygcn	180
ttyggngara	arcaygayaa	ytgyacnacr	aaywsnwsna	cnwsngaraa	ymngncnwsn	240
tgysnttyt	tyytnccnm	nathacnath	ccngayaayt	ayacnathga	rgtnngargcn	300
garaayggng	ayggngtnat	haarwsncay	atgacntayt	ggmgnytnga	raayathgcn	360
aaracngarc	cncnnaarat	htymngntn	aarccngtny	tnngnathaa	rmgnatgath	420
carathgart	ggathaarcc	ngarytnngcn	ccngtnwsnw	sngayytnaa	rtayacnytn	480
mgnttymgna	cngtnaayws	nacnwsntgg	atggargtna	aytytgcnaa	raaymgnaar	540
gayaaraayc	aracntayaa	yytnacnggn	ytnarccnt	tyacngarta	ygtnathgcn	600
ytnmgntgyg	cngtnaarga	rsnnaartty	tggwsngayt	ggwsncarga	raaratgggn	660
atgacngarg	argargcncc	ntgyggnytn	garytnntggm	gngtnytnaa	rccngcngar	720
gcngayggng	gnmgncngt	nmgnytnytn	tggaaraarg	cnmgnggngc	nccngtnytn	780
garaaracny	tnngntayaa	yathtggtay	tayccngarw	snaayacnaa	yytnacngar	840
acnatgaaya	cnacnaayca	rcarytngar	ytncayytn	gnggngarws	nttytgggt	900
wsnatgathw	sntayaayws	nytnnggnaar	wsnccngtn	cnacnytnmg	nathccngcn	960

athcargara arwsnttyca rtgyathgar gtnatgcarg cntgygtngc ngargaycar 1020
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 ccngaygtng aywsngarcc nacnacnytn wsntgggarw sngtnwsnca rgnacnaay 1140
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 atgytncayg ayaargtngg ngarccntay wsnathcarg cntaygcnaa rgarggngtn 1260
 ccnwsngarg gncngarac naargtngar aayathggng tnaaracngt nacnathacn 1320
 tggaargara thccnaarws ngarmgnaar ggnathatht gyaaytayac nathttytay 1380
 cargcngarg gnggnaargg nttywsnaar acngtnaayw snwsnathyt ncartaygg 1440
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 athytnatha cnwsnytnat hggnggnggn ytnytnathy tnathathyt nacngtngcn 1620
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 gcngarwsnw snathgcnac ntggcayggg gaygayttya argayaaryt naayytnaar 1740
 garwsngayg aywsngtnaa yacngargay mgnathytna arccntgyws nacccnwsn 1800
 gayaarytng tnathgayaa rytngtngtn aayttyggna aygtnytnca rgarathtty 1860
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<211> 32

<212> PRT

<213> Homo sapiens

<400> 48

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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21195

<400> 49

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<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC21196

<400> 50

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<210> 51

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27900

<400> 51

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<210> 52

<211> 13

<212> PRT

<213> Homo sapiens

<400> 52

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1 5 10

<210> 53

<211> 2903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (497)...(2482)

<400> 53

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gaatgtccgc	aaaacattag	tttactctt	gtcgccagg	tggagtacaa	tggcacgac	180
ttggctcact	gcaacctctg	cctccgggt	tcaagcgatt	ctcctgcctc	agcctccga	240
gtagctggga	ttacagttaa	caataatgca	atccatttcc	cagcataagt	gggtaagtgc	300

tgg ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca	1012
Trp Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr	
160 165 170	
ctt cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc	1060
Leu Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe	
175 180 185	
gct aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg	1108
Ala Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu	
190 195 200	
cag cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag	1156
Gln Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu	
205 210 215 220	
tca aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag	1204
Ser Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu	
225 230 235	
gaa gaa gct cca tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct	1252
Glu Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala	
240 245 250	
gag gcg gat gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga	1300
Glu Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg	
255 260 265	
gga gcc cca gtc cta gag aaa aca ctt ggc tac aac ata tgg tac tat	1348
Gly Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr	
270 275 280	
cca gaa agc aac act aac ctc aca gaa aca atg aac act act aac cag	1396
Pro Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln	
285 290 295 300	
cag ctt gaa ctg cat ctg gga ggc gag agc ttt tgg gtg tct atg att	1444
Gln Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile	
305 310 315	
tct tat aat tct ctt ggg aag tct cca gtg gcc acc ctg agg att cca	1492
Ser Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro	
320 325 330	

Gly	Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	
	495						500					505				
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Ala	Ser	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	
	510					515					520					
aca	ttg	tca	ttc	agt	gtc	ttt	gag	att	atc	ctc	ata	act	tct	ctg	att	2116
Thr	Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	
525					530					535					540	
ggt	gga	ggc	ctt	ctt	att	ctc	att	atc	ctg	aca	gtg	gca	tat	ggt	ctc	2164
Gly	Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	
				545					550					555		
aaa	aaa	ccc	aac	aaa	ttg	act	cat	ctg	tgt	tgg	ccc	acc	gtt	ccc	aac	2212
Lys	Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	
			560					565					570			
cct	gct	gaa	agt	agt	ata	gcc	aca	tgg	cat	gga	gat	gat	ttc	aag	gat	2260
Pro	Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	
		575					580					585				
aag	cta	aac	ctg	aag	gag	tct	gat	gac	tct	gtg	aac	aca	gaa	gac	agg	2308
Lys	Leu	Asn	Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	
	590					595					600					
atc	tta	aaa	cca	tgt	tcc	acc	ccc	agt	gac	aag	ttg	gtg	att	gac	aag	2356
Ile	Leu	Lys	Pro	Cys	Ser	Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	
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ttg	gtg	gtg	aac	ttt	ggg	aat	gtt	ctg	caa	gaa	att	ttc	aca	gat	gaa	2404
Leu	Val	Val	Asn	Phe	Gly	Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	
			625					630						635		
gcc	aga	acg	ggt	cag	gaa	aac	aat	tta	gga	ggg	gaa	aag	aat	ggg	act	2452
Ala	Arg	Thr	Gly	Gln	Glu	Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	
			640					645					650			
aga	att	ctg	tct	tcc	tgc	cca	act	tca	ata	taagtgtgga	ctaaaatgcg					2502
Arg	Ile	Leu	Ser	Ser	Cys	Pro	Thr	Ser	Ile							
		655				660										

Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
 225 230 235 240
 Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly
 245 250 255
 Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
 260 265 270
 Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn
 275 280 285
 Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
 290 295 300
 His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
 305 310 315 320
 Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
 325 330 335
 Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
 340 345 350
 Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
 355 360 365
 Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
 370 375 380
 Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
 385 390 395 400
 Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
 405 410 415
 Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
 420 425 430
 Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
 435 440 445
 Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly
 450 455 460
 Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
 465 470 475 480
 Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
 485 490 495
 Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser
 500 505 510
 Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
 515 520 525
 Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
 530 535 540
 Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
 545 550 555 560

Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser
 565 570 575
 Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
 580 585 590
 Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
 595 600 605
 Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
 610 615 620
 Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
 625 630 635 640
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 Ser Cys Pro Thr Ser Ile
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<211> 1986

<212> DNA

<213> Artificial Sequence

<220>

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<221> misc_feature

<222> (1)...(1986)

<223> n = A,T,C or G

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athwsntgyg	tntaytayta	ymgnaaraay	ytnactgya	cntggwsncc	nggnaargar	180
acnwsntaya	cncartayac	ngtnaarmgn	acntaygcnt	tyggngaraa	rcaygayaay	240
tgyacnacna	aywsnwnac	nwsngaraay	mgngcnwsnt	gywsnttytt	yytnccnmgn	300
athacnathc	cngayaayta	yacnathgar	gtngargcng	araayggnga	yggngtnath	360
aarwsncaya	tgacntaytg	gmgnytngar	aayathgcna	aracngarcc	nccnaarath	420
ttymgngtna	arccngtnyt	nggnathaar	mgnatgathc	arathgartg	gathaarccn	480
garytngcnc	cngtnwsnws	ngayytnaar	tayacnytnm	gnttymgnac	ngtnaaywsn	540
acnwsntgga	tggargtnaa	ytygcnaar	aaymgnaarg	ayaaraayca	racntayaay	600
ytnacnggny	tncarccntt	yacngartay	gtnathgcny	tnmgntgygc	ngtnaargar	660
wsnaarttyt	ggwsngaytg	gwsncargar	aatatgggna	tgacngarga	rgargcnccn	720
tgyggnytn	arytnctggmg	ngtnytnaar	ccngcngarg	cngayggnmg	nmgncngtn	780
mgnytnytnt	ggaaraargc	nmgngngcnc	ccngtnytng	araaracnyt	nggntayaay	840

athtggtayt ayccngarws naayacnaay ytnacngara cnatgaayac nacnaaycar 900
 carytngary tncayytngg nggngarwsn ttytggtgnw snatgathws ntayaaywsn 960
 ytnngnaarw snccngtngc nacnytnmgn athccngcna thcargaraa rwsnttycar 1020
 tgyathgarg tnatgcargc ntgygtngcn gargaycary tngtngtnaa rtggcarwsn 1080
 wsngcnytn gytgnaayac ntggatgath gartggttyc cngaygtnga ywsngarccn 1140
 acnacnytnw sntgggarws ngtnwsncar gcnacnaayt ggacnathca rcargayaar 1200
 ytnaarcnt tytggtyta yaayathwsn gtnayccna tgytncaiga yaargtnggn 1260
 garccntayw snathcargc ntaygcnaar gargngtnc cnwsngargg nccngaracn 1320
 aargtngara ayathggngt naaracngtn acnathacnt ggaargarat hccnaarwsn 1380
 garmgnaarg gnathathtg yaaytayacn athtityc argcngargg nggnaarggn 1440
 ttywsnaara cngtnaayws nwsnathytn cartayggny tngarwsnyt naarmgnaar 1500
 acnwsntaya thgtncargt natggcnwsn acnwsngcng gnggnacnaa ygggnacnwsn 1560
 athaaytaya aracnytnws nttywsngtn ttygaratha thytnathac nwsnytnath 1620
 ggngggngny tnytnathyt nathathytn acngtngcnt ayggnytnaa raarccnaay 1680
 aarytnacnc ayytntgytg gccnacngtn ccnaayccng cngarwsnws nathgcnacn 1740
 tggcayggng aygayttaa rgayaarytn aayytnaarg arwsngayga ywsngtnaay 1800
 acngargaym gnathytnaa rccntgywsn acnccnwsng ayaarytngt nathgayaar 1860
 ytngtngtna aytyggnaa ygtnytnar garathtitya cngaygargc nmgnacnggn 1920
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<211> 2748

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<213> mus musculus

<220>

<221> CDS

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 ctctcagaga aggcagtgtt ggaggcggtc ctggcccggg tctcctccta ctgttcctgg 180
 tagcccagcc ttctcggggg ggaaggagaa gctggccagg tgagctctga ggaagc atg 239
 Met
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ctg agc agc cag aag gga tcc tgc agc cag gaa cca ggg gca gcc cac 287
 Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala His
 5 10 15

gtc cag cct ctg ggt gtg aac gct gga ata atg tgg acc ttg gca ctg 335

Val	Gln	Pro	Leu	Gly	Val	Asn	Ala	Gly	Ile	Met	Trp	Thr	Leu	Ala	Leu		
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tgg	gca	ttc	tct	ttc	ctc	tgc	aaa	ttc	agc	ctg	gca	gtc	ctg	ccg	act		383
Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	Thr		
	35					40				45							
aag	cca	gag	aac	att	tcc	tgc	gtc	ttt	tac	ttc	gac	aga	aat	ctg	act		431
Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	Thr		
	50				55				60					65			
tgc	act	tgg	aga	cca	gag	aag	gaa	acc	aat	gat	acc	agc	tac	att	gtg		479
Cys	Thr	Trp	Arg	Pro	Glu	Lys	Glu	Thr	Asn	Asp	Thr	Ser	Tyr	Ile	Val		
				70				75						80			
act	ttg	act	tac	tcc	tat	gga	aaa	agc	aat	tat	agt	gac	aat	gct	aca		527
Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	Thr		
			85				90					95					
gag	gct	tca	tat	tct	ttt	ccc	cgt	tcc	tgt	gca	atg	ccc	cca	gac	atc		575
Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	Ile		
	100					105				110							
tgc	agt	gtt	gaa	gta	caa	gct	caa	aat	gga	gat	ggt	aaa	gtt	aaa	tct		623
Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	Ser		
	115				120				125								
gac	atc	aca	tat	tgg	cat	tta	atc	tcc	ata	gca	aaa	acc	gaa	cca	cct		671
Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	Pro		
	130				135				140					145			
ata	att	tta	agt	gtg	aat	cca	att	tgt	aat	aga	atg	ttc	cag	ata	caa		719
Ile	Ile	Leu	Ser	Val	Asn	Pro	Ile	Cys	Asn	Arg	Met	Phe	Gln	Ile	Gln		
			150					155					160				
tgg	aaa	ccg	cgt	gaa	aag	act	cgt	ggg	ttt	cct	tta	gta	tgc	atg	ctt		767
Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	Leu		
		165					170					175					
cgg	ttc	aga	act	gtc	aac	agt	agc	cgc	tgg	acg	gaa	gtc	aat	ttt	gaa		815
Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	Glu		
	180					185						190					

aac tgt aaa cag gtc tgc aac ctc aca gga ctt cag gct ttc aca gaa	863
Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr Glu	
195 200 205	
tat gtc ctg gct cta cga ttc agg ttc aat gac tca aga tat tgg agc	911
Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp Ser	
210 215 220 225	
aag tgg agc aaa gaa gaa acc aga gtg act atg gag gaa gtt cca cat	959
Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro His	
230 235 240	
gtc ctg gac ctg tgg aga att ctg gaa cca gca gac atg aac gga gac	1007
Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly Asp	
245 250 255	
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Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu	
260 265 270	
gag aaa aca ttt ggc tac cac ata cag tac ttt gca gag aac agc act	1103
Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser Thr	
275 280 285	
aac ctc aca gag ata aac aac atc acc acc cag cag tat gaa ctg ctt	1151
Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu Leu	
290 295 300 305	
ctg atg agc cag gca cac tct gtg tcc gtg act tct ttt aat tct ctt	1199
Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser Leu	
310 315 320	
ggc aag tcc caa gag acc atc ctg agg atc cca gat gtc cat gag aag	1247
Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu Lys	
325 330 335	
acc ttc cag tac att aag agc atg cag gcc tac ata gcc gag ccc ctg	1295
Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro Leu	
340 345 350	
ttg gtg gtg aac tgg caa agc tcc att cct gcg gtg gac act tgg ata	1343
Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp Ile	
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<211> 662

<212> PRT

<213> mus musculus

<400> 57

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Leu	Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	
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Thr	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	
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65				70						75				80		
Val	Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	
			85					90					95			
Thr	Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	
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Ile	Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	
	115					120				125						
Ser	Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	
130					135					140						
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Gln	Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	
			165					170					175			
Leu	Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	
		180					185					190				
Glu	Asn	Cys	Lys	Gln	Val	Cys	Asn	Leu	Thr	Gly	Leu	Gln	Ala	Phe	Thr	
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210					215					220						
Ser	Lys	Trp	Ser	Lys	Glu	Glu	Thr	Arg	Val	Thr	Met	Glu	Glu	Val	Pro	
225				230						235				240		
His	Val	Leu	Asp	Leu	Trp	Arg	Ile	Leu	Glu	Pro	Ala	Asp	Met	Asn	Gly	
			245					250					255			
Asp	Arg	Lys	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	
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 275 280 285
 Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu
 290 295 300
 Leu Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser
 305 310 315 320
 Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
 325 330 335
 Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
 340 345 350
 Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
 355 360 365
 Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
 370 375 380
 Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp
 385 390 395 400
 Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
 405 410 415
 Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu
 420 425 430
 Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu
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 Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn
 450 455 460
 Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys
 465 470 475 480
 Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu
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 Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr
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 Asn Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu
 565 570 575
 Ser Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met
 580 585 590
 Lys Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro
 595 600 605

Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu
 610 615 620
 Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala
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<220>
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<210> 64
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 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC27895

<400> 64
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<210> 65
 <211> 34
 <212> DNA
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 <223> Oligonucleotide primer ZC29122

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 ccgctcgagt tatattgaag ttgggcagga agac 34

<210> 66
 <211> 33
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC29451

<400> 66
 ccggaattcc cctgatacat gaagctctct ccc 33

<210> 67
 <211> 33
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<220>
 <223> Oligonucleotide primer ZC29124

<400> 67
 cgcgatccc tcaaagacac tgaatgacaa tgt 33

<210> 68
 <211> 2295
 <212> DNA
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<220>
 <223> Polynucleotide encoding human zcytor17-Fc4 fusion

<221> CDS

<222> (1)...(2295)

<400> 68

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Met	Lys	Leu	Ser	Pro	Gln	Pro	Ser	Cys	Val	Asn	Leu	Gly	Met	Met	Trp	
1				5					10					15		

acc	tgg	gca	ctg	tgg	atg	ctc	cct	tca	ctc	tgc	aaa	ttc	agc	ctg	gca	96
Thr	Trp	Ala	Leu	Trp	Met	Leu	Pro	Ser	Leu	Cys	Lys	Phe	Ser	Leu	Ala	
			20					25					30			

gct	ctg	cca	gct	aag	cct	gag	aac	att	tcc	tgt	gtc	tac	tac	tat	agg	144
Ala	Leu	Pro	Ala	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Tyr	Tyr	Tyr	Arg	
		35				40					45					

aaa	aat	tta	acc	tgc	act	tgg	agt	cca	gga	aag	gaa	acc	agt	tat	acc	192
Lys	Asn	Leu	Thr	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr	Ser	Tyr	Thr	
	50					55					60					

cag	tac	aca	gtt	aag	aga	act	tac	gct	ttt	gga	gaa	aaa	cat	gat	aat	240
Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys	His	Asp	Asn	
65					70					75					80	

tgt	aca	acc	aat	agt	tct	aca	agt	gaa	aat	cgt	gct	tcg	tgc	tct	ttt	288
Cys	Thr	Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	
				85					90					95		

ttc	ctt	cca	aga	ata	acg	atc	cca	gat	aat	tat	acc	att	gag	gtg	gaa	336
Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	
			100					105					110			

gct	gaa	aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	384
Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	
		115				120						125				

tta	gag	aac	ata	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	432
Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	
		130				135					140					

cca	gtt	ttg	ggc	atc	aaa	cga	atg	att	caa	att	gaa	tgg	ata	aag	cct	480
Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	
145					150				155						160	

T09290"6762680

aaa tca ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac	1056
Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp	
340 345 350	
cag cta gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg	1104
Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp	
355 360 365	
atg att gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc	1152
Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser	
370 375 380	
tgg gaa tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa	1200
Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys	
385 390 395 400	
tta aaa ccc ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat	1248
Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His	
405 410 415	
gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc	1296
Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
420 425 430	
gtt cca tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag	1344
Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys	
435 440 445	
acg gtc acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt	1392
Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly	
450 455 460	
atc atc tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga	1440
Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly	
465 470 475 480	
ttc tcc aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc	1488
Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser	
485 490 495	
ctg aaa cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt	1536

Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser	
500 505 510	
gct ggg gga acc aac ggg acc agc ata aat ttc aag aca ttg tca ttc	1584
Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe	
515 520 525	
agt gtc ttt gag gag ccc aga tct tca gac aaa act cac aca tgc cca	1632
Ser Val Phe Glu Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro	
530 535 540	
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc	1680
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	
545 550 555 560	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	1728
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
565 570 575	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	1776
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
580 585 590	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	1824
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
595 600 605	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	1872
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
610 615 620	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1920
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
625 630 635 640	
tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc	1968
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala	
645 650 655	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	2016
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
660 665 670	

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 2064
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 675 680 685

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 2112
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 690 695 700

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 2160
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 705 710 715 720

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 2208
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 725 730 735

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 2256
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 740 745 750

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taa 2295
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
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<211> 764

<212> PRT

<213> Artificial Sequence

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<400> 69

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 20 25 30
 Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
 35 40 45
 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
 50 55 60

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 740 745 750
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 755 760

<210> 70
 <211> 34
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC29157

<400> 70
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<210> 71
 <211> 41
 <212> DNA
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<400> 71
 gtctgaagat ctgggctcct caaagacact gaatgacaat g 41

<210> 72
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<220>
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<400> 72
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<210> 73
 <211> 20
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<220>

<223> Oligonucleotide primer ZC28917

<400> 73

tgcaagatgc tggaattgac

20

<210> 74

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC29179

<400> 74

gcagggttgg gaacggtgg

19

<210> 75

<211> 20

<212> DNA

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<223> Oligonucleotide primer ZC28916

<400> 75

agtcaattcc agcatcttgc

20

<210> 76

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC28918

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20

<210> 77

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38065

<400> 77

ctttcctggg aatctgtgtc t

21

<210> 78

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38068

<400> 78

cctccagctc tgggtgctg

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<223> Oligonucleotide primer ZC10651

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<223> Oligonucleotide primer ZC10565

<400> 80

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<210> 81

<211> 24

<212> DNA
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<400> 81
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<210> 82
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<400> 82
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<210> 83
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<220>
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 probe

<400> 83
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<210> 84
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<220>
 <223> rRNA forward primer

<400> 84
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<210> 85
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<220>
 <223> rRNA reverse primer

<400> 85
 gctggaatta ccgcggct 18

<210> 86
 <211> 22
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<220>
 <223> rRNA TaqMan® probe

<400> 86
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<210> 87
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<210> 88
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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC38239

<400> 88
 gccgactaag ccagagaac 19

<210> 89
 <211> 20
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<220>
 <223> Oligonucleotide primer ZC38245

<400> 89
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<210> 90
 <211> 20
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<220>
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<400> 90
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<210> 91
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<220>
 <223> Modified Glu-Glu tag peptide

<400> 91
 Gly Ser Glu Tyr Met Pro Met Glu
 1 5

<210> 92
 <211> 2728
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (237)...(1877)

<400> 92

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 ctctcagaga aggcagtgct ggaggcgttc ctggcccggg tctcctccta ctgttcctgg 180
 tagcccagcc ttctcggggt ggaaggagaa gctggccagg tgagctctga ggaagc atg 239
 Met
 1

ctg agc agc cag aag gga tcc tgc agc cag gaa cca ggg gca gcc cac 287
 Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala His
 5 10 15

gtc cag cct ctg ggt gtg aac gct gga ata atg tgg acc ttg gca ctg 335
 Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu
 20 25 30

tgg gca ttc tct ttc ctc tgc aaa ttc agc ctg gca gtc ctg ccg act 383
 Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro Thr
 35 40 45

aag cca gag aac att tcc tgc gtc ttt tac ttc gac aga aat ctg act 431
 Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu Thr
 50 55 60 65

tgc act tgg aga cca gag aag gaa acc aat gat acc agc tac att gtg 479
 Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile Val
 70 75 80

act ttg act tac tcc tat gga aaa agc aat tat agt gac aat gct aca 527
 Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala Thr
 85 90 95

gag gct tca tat tct ttt ccc cgt tcc tgt gca atg ccc cca gac atc 575
 Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp Ile
 100 105 110

tgc agt gtt gaa gta caa gct caa aat gga gat ggt aaa gtt aaa tct 623
 Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys Ser
 115 120 125

gac atc aca tat tgg cat tta atc tcc ata gca aaa acc gaa cca cct 671

ctg atg agc cag gca cac tct gtg tcc gtg act tct ttt aat tct ctt	1199
Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser Leu	
310 315 320	
ggc aag tcc caa gag acc atc ctg agg atc cca gat gtc cat gag aag	1247
Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu Lys	
325 330 335	
acc ttc cag tac att aag agc atg cag gcc tac ata gcc gag ccc ctg	1295
Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro Leu	
340 345 350	
ttg gtg gtg aac tgg caa agc tcc att cct gcg gtg gac act tgg ata	1343
Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp Ile	
355 360 365	
gtg gag tgg ctc cca gaa gct gcc atg tcg aag ttc cct gcc ctt tcc	1391
Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu Ser	
370 375 380 385	
tgg gaa tct gtg tct cag gtc acg aac tgg acc atc gag caa gat aaa	1439
Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp Lys	
390 395 400	
cta aaa cct ttc aca tgc tat aat ata tca gtg tat cca gtg ttg gga	1487
Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu Gly	
405 410 415	
cac cga gtt gga gag ccg tat tca atc caa gct tat gcc aaa gaa gga	1535
His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
420 425 430	
act cca tta aaa ggt cct gag acc agg gtg gag aac atc ggt ctg agg	1583
Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu Arg	
435 440 445	
aca gcc acg atc aca tgg aag gag att cct aag agt gct agg aat gga	1631
Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn Gly	
450 455 460 465	
ttt atc aac aat tac act gta ttt tac caa gct gaa ggt gga aaa gaa	1679

Met	Leu	Ser	Ser	Gln	Lys	Gly	Ser	Cys	Ser	Gln	Glu	Pro	Gly	Ala	Ala	
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His	Val	Gln	Pro	Leu	Gly	Val	Asn	Ala	Gly	Ile	Met	Trp	Thr	Leu	Ala	
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Leu	Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	
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Thr	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	
	50					55					60					
Thr	Cys	Thr	Trp	Arg	Pro	Glu	Lys	Glu	Thr	Asn	Asp	Thr	Ser	Tyr	Ile	
65					70					75					80	
Val	Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	
				85					90					95		
Thr	Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	
			100					105					110			
Ile	Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	
		115					120					125				
Ser	Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	
	130					135					140					
Pro	Ile	Ile	Leu	Ser	Val	Asn	Pro	Ile	Cys	Asn	Arg	Met	Phe	Gln	Ile	
145					150					155					160	
Gln	Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	
				165					170					175		
Leu	Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	
			180					185					190			
Glu	Asn	Cys	Lys	Gln	Val	Cys	Asn	Leu	Thr	Gly	Leu	Gln	Ala	Phe	Thr	
		195					200					205				
Glu	Tyr	Val	Leu	Ala	Leu	Arg	Phe	Arg	Phe	Asn	Asp	Ser	Arg	Tyr	Trp	
	210					215					220					
Ser	Lys	Trp	Ser	Lys	Glu	Glu	Thr	Arg	Val	Thr	Met	Glu	Glu	Val	Pro	
225					230						235				240	
His	Val	Leu	Asp	Leu	Trp	Arg	Ile	Leu	Glu	Pro	Ala	Asp	Met	Asn	Gly	
				245					250					255		
Asp	Arg	Lys	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	
			260					265					270			
Leu	Glu	Lys	Thr	Phe	Gly	Tyr	His	Ile	Gln	Tyr	Phe	Ala	Glu	Asn	Ser	
		275					280					285				
Thr	Asn	Leu	Thr	Glu	Ile	Asn	Asn	Ile	Thr	Thr	Gln	Gln	Tyr	Glu	Leu	
	290					295					300					
Leu	Leu	Met	Ser	Gln	Ala	His	Ser	Val	Ser	Val	Thr	Ser	Phe	Asn	Ser	
305					310						315				320	
Leu	Gly	Lys	Ser	Gln	Glu	Thr	Ile	Leu	Arg	Ile	Pro	Asp	Val	His	Glu	
				325					330					335		

